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1GCGA 4
1 CTCGGGTAACCTTCTTGAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 50
5 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 54
51 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 100
55 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 104
101 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 150
105 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 154
151 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCATAATATCTG 200
155 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 204
201 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 250
205 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 254
251 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 300
255 GGATAGCTGGGTTACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 304
301 GGATAGCTGGGTTACGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 350
305 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 354
351 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 400
355 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 404
401 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 450
405 CCTCCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 454
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500
455 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 504
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
505 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 554
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
555 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 604
601 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650

Fig. 1A

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605 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 654
|||||
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCCGCATG 700
|||||
655 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 704
|||||
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750
|||||
705 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGGAACGGCTG 754
|||||
751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGGAACGGCTG 800
|||||
755 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 804
|||||
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850
|||||
805 GGAGGTTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 854
|||||
851 GGAGGTTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
|||||
855 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 904
|||||
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950
|||||
905 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 954
|||||
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000
|||||
955 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGGATGAGCGTCT 1004
|||||
1001 ATGAGTCCCGCCGAGTACATGGAGTGTTACGGACTCTTGGATGAGCGTCT 1050
|||||
1005 GCAGGTTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTCCGGCTGCTGC 1054
|||||
1051 GCAGGTTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTCCGGCTGCTGC 1100
|||||
1055 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1104
|||||
1101 ACCGCCACAATGTGAAGGTCGCGTCGCAGGTTGTGAGCAATGCCTACCTC 1150
|||||
1105 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGCATGGCCGT 1154
|||||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGCATGGCCGT 1200
|||||
1155 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAACATGATCG 1204
|||||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1250
|||||
1205 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1254
|||||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300
|||||

Fig 1B

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1255 GACGTGCTGACCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1304
|||||
1301 GACGTGCTGACCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350
|||||
1305 GCGTTCGTTGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1354
|||||
1351 GCGTTCGTTGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400
|||||
1355 GCGCGGACCTTATCCTGCTTGACCTGCGTCA CCTCAGACGACTCCTCAC 1404
|||||
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCA CCTCAGACGACTC TCA 1447
|||||
1405 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1454
|||||
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497
|||||
1455 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1504
|||||
1498 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547
|||||
1505 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1554
|||||
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597
|||||
1555 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1604
|||||
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCAGCTTGCGG 1647
|||||
1605 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1654
|||||
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697
|||||
1655 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1704
|||||
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747
|||||
1705 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1754
|||||
1748 GGATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797
|||||
1755 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1804
|||||
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847
|||||
1805 AAAG..... 1808
|||||
1848 AAAGCCCCGAG 1858

Fig. 1C

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1GAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 35
1 CTCGGGTAACCTTCTTGAGCGCGGCCACAGCAGCCTTGATCATGAAGGCGA 50
36 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 85
51 GCATGGTGACCTTGACGCCGCTCTTTTCGTTCTCTTTGTTGAACTGCACG 100
86 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 135
101 CGAAAGGCTTCCAGGTCGGTGATGTCCGCGTCGTCGTGGTTGGTGACGTG 150
136 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCGTAATATCTG 185
151 CGGGATGACCACCCAGTTGCGGTGCAGGTTTTTCGATGGCGTAATATCTG 200
186 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 235
201 CGTTGCGACGTGTAACACACTATTGGAGACATATCATGCAAACGCTCAGC 250
236 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 285
251 ATCCAGCACGGTACCCTCGTCACGATGGATCAGTACCGCAGAGTCCTTGG 300
286 GGATAGCTGGGTTACAGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 335
301 GGATAGCTGGGTTACAGTGCAGGATGGACGGATCGTCGCGCTCGGAGTGC 350
336 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 385
351 ACGCCGAGTCGGTGCCTCCGCCAGCGGATCGGGTGATCGATGCACGCGGC 400
386 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 435
401 AAGGTCGTGTTACCCGGTTTCATCAATGCCACACCCATGTGAACCAGAT 450
436 CCTCCTGCGCGGAGGGCCCTCGCACGGCGTCAATTCTATGACTGGCTGT 485
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500
486 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 535
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
536 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 585
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
586 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 635
601 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650

Fig. 2A

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636 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 685
|||||
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700
686 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 735
|||||
701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750
736 GGCTCGCTCTCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 785
|||||
751 GGCTCGCTCTCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800
786 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 835
|||||
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850
836 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 885
|||||
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
886 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCGTGATCGGGCGGTAA 935
|||||
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCGTGATCGGGCGGTAA 950
936 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 985
|||||
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000
986 ATGAGTCCCGCCGATTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1035
|||||
1001 ATGAGTCCCGCCGATTACATGGAGTGTTACGGACTCTTGATGAGCGTCT 1050
1036 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTTCGGCTGCTGC 1085
|||||
1051 GCAGGTCGCGCATTGCGTGTACTTTGACCGGAAGGATGTTTCGGCTGCTGC 1100
1086 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1135
|||||
1101 ACCGCCACAATGTGAAGGTCGCGTCGAGGTTGTGAGCAATGCCTACCTC 1150
1136 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1185
|||||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200
1186 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1235
|||||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 1250
1236 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1285
|||||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

Fig. 2B

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1286 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1335
|||||
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350
|||||
1336 GCGTTCGTTGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1385
|||||
1351 GCGTTCGTTGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAGC 1400
|||||
1386 GCGCGGACCTTATCCTGCTTGACCTGCGTCACCTCAGACGACTCCTCAC 1435
|||||
1401 GCGCGGACCTTATCCTGCTTGACCTGCGTCACTCAGACGACTCTCA 1447
|||||
1436 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1485
|||||
1448 CATCATTTGGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGGA 1497
|||||
1486 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1535
|||||
1498 CACTGTCCTGATTGACGGAACGTTGTGATGGAGAACCGCCGCTTGAGCT 1547
|||||
1536 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1585
|||||
1548 TTCTTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGC 1597
|||||
1586 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1635
|||||
1598 GCCACAGCTATTTTGCAGCGGGCGAACATGGTGGCTAACCCAGCTTGGCG 1647
|||||
1636 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1685
|||||
1648 CAGCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAA 1697
|||||
1686 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1735
|||||
1698 TCGCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGAT 1747
|||||
1736 GGATACAGAAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1785
|||||
1748 GGATACAGAAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGA 1797
|||||
1786 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1835
|||||
1798 ATCGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGTG 1847
|||||
1836 AAAGGCCCCGAG 1846
|||||
1848 AAAGGCCCCGAG 1858

Fig. 2C

Fig. 3

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1 SAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVTCT 45
 1 SGNFLSAATAALIMKASMTLTPLFSFSLNCTRKASRSVMSASSWLVTCT 50
 46 GMTTQLRCRFFDGVISALRRVTHYWRHIMOTLSIQHGTLVTMDQYRRVLG 95
 51 GMTTQLRCRFFDGVISALRRVTHYWRHIMOTLSIQHGTLVTMDQYRRVLG 100
 96 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 145
 101 DSWVHVQDGRIVALGVHAESVPPPADRVIDARGKVVLPGFINAHTHVNQI 150
 146 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 195
 151 LLRGGPSHGRQFYDWLFNVVYPGQKAMPEDVAVAVRLYCAEAVRSGITT 200
 196 INENADSAIYPGNIEAAMAVYGEVGVRVVYARMFFDRMDGRIQGYVDALK 245
 201 INENADSAIYPGNIEAAMAVYGEVGVRVVYARMFFDRMDGRIQGYVDALK 250
 246 ARSPQVELCSIMEETAVAKDRITALSDQYHGTTAGGRISVWPAPATTTAVT 295
 251 ARSPQVELCSIMEETAVAKDRITALSDQYHGTTAGGRISVWPAPATTTAVT 300
 296 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPADYMECYGLLDERL 345
 301 VEGMRWAQAFARDRAVMWTLHMAESDHDERIHGMSPAEMYMECYGLLDERL 350
 346 QVAHCVYFDRKDVRLLRHNVKVASQVVSNAYLGSQVAPVPEMVERGMAV 395
 351 QVAHCVYFDRKDVRLLRHNVKVASQVVSNAYLGSQVAPVPEMVERGMAV 400
 396 GIGTDNGNSNDSVNMIGDMKFMAHIHRAVHRDADVLTPKILEMATIDGA 445
 401 GIGTDNGNSNDSANMIGDMKFMAHIHRAVHRDADVLTPKILEMATIDGA 450
 446 RSLGMDHEIGSIETGKRADLILLDLRHPOTTPHHHLAATIVFQAYGNEVD 495
 451 RSLGMDHEIGSIETGKRADLILLDLRHLLRRLS.HHLAATIVFQAYGNEVD 499
 496 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 545
 500 TVLIDGNVVMENRRLSFLPPERELAFLEEAQSRATAILQRANMVANPAWR 549
 STOP
 546 SI*EMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 595
 550 SI*EMTPLLHPPPLEEIAAILARLGLGGGHDLDGYRIAMNAALPSFARVE 599
 596 SLVGEGRRLAPASRRSERPE 615
 600 SLVGEGRRLAPASRRGERPE 619

Fig. 4

Fig. 5A

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1 ...CCTGCGCGGAGGGCCCTCGCACGGGCGTCAATTCTATGACTGGCTGT 47
 451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500
 48 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 97
 501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
 98 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 147
 551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
 148 GATCAACGAAAACNCCGATTCTGGCCATCTACCCAGGCAACATCGAGGCCG 197
 601 GATCAACGAAAACGCCGATTCTGGCCATCTACCCAGGCAACATCGAGGCCG 650
 198 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 247
 651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700
 248 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 297
 701 TTCTTTGATCGGATGGACGGGCGCATTCAAGGGTATGTGGACGCCTTGAA 750
 298 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGANGAAACNGCTG 347
 751 GGCTCGCTCTCCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800
 348 TGGCCAAAGATCGGATCACANCCCTGT CANATCANTATCATGGCACNGCA 397
 801 TGGCCAAAGATCGGATCACAGCCCTGT CAGATCAGTATCATGGCACGGCA 850
 398 NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 447
 851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
 448 ATTTAAANGAATCCATGGGCCA...ACCTCCCCCGTGATCCGGCGGTAA 493
 901 ACTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCGTGATCGGGCGGTAA 950
 494 TGTGAC..... 499
 951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTTCATGGG 1000

Fig. 5B

```

360 .....TNGCAGGTTGTGAGCA..TGCTACTTC 336
      |:||||||||||||| |||||
1101 ACCGCCACAATGTGAAGTCTCGCTCGCAGGTTGTGAGCAATGCCTACCTC 1150

      .
335 GGTTCAGGNGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 286
      || |||||:|||||||||||||||||||||||||||||||||||||
1151 GGCTCAGGGGTGGCCCCCGTGCCAGAGATGGTGGAGCGCGGCATGGCCGT 1200

      .
285 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGTAAACATGATCG 236
      |||||||||||||||||||||||||||||||||||||||||||||
1201 GGGCATTGGAACAGATAACGGGAATAGTAATGACTCCGCAAACATGATCG 1250

      .
235 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 186
      |||||||||||||||||||||||||||||||||||||||||||||
1251 GAGACATGAAGTTTATGGCCCATATTCACCGCGCGGTGCATCGGGATGCG 1300

      .
185 GACGTGCTGACCCCAGAGAAGATTNTTGAAATGGCGACGATCGATGGGGC 136
      |||||||||||||||||||:|||||||||||||||||
1301 GACGTGCTGACCCCAGAGAAGATTCTTGAAATGGCGACGATCGATGGGGC 1350

      .
135 GCGTTTCGTTGGGGATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 86
      ||| ||||||||||||||| |||||
1351 GCG.TTCGTTGGGAATGGACCACGAGATTGGTTCCATCGAAACCGGCAAG 1399

      .
85 CGCGCGGACCTTATCCTGCTTGACCTGCGTCACCCTCAGACGACTCCTCA 36
      ||||| ||||||||||| |||||
1400 CGCGCGGACCTTATCCTGCTTGACCTGCGTCA.CCTCAGACGACTC..TC 1446

      .
35 CCATCATTGCGGCCACGATCGTGTTTCAGGCTT..... 1
      ||||||||||||||| |||||
1447 ACATCATTGCGGCCACGATCGTGTTTCAGGCTTACGGCAATGAGGTGG 1496

```

Fig. 5C

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1CGGCCACGATCGTGTTCAGGCTTACGGCAATGAGGTGGACAC 43
|||||
1451 CATTTGGCGGCCACGATCGTGTTCAGGCTTACGGCAATGAGGTGGACAC 1500
44 TGTCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCTTTC 93
|||||
1501 TGTCTGATTGACGGAAACGTTGTGATGGAGAACCGCCGCTTGAGCTTTC 1550
94 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 143
|||||
1551 TTCCCCCTGAACGTGAGTTGGCGTTCCTTGAGGAAGCGCAGAGCCGCGCC 1600
144 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 193
|||||
1601 ACAGCTATTTTGCATCGGGCGAAACATGGTGGCTAACCCAGCTTGGCGCA 1649
194 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 243
|||||
1650 GCCTCTAGGAAATGACGCCGTTGCTGCATCCGCCGCCCTTGAGGAAATC 1699
244 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 293
|||||
1700 GCTGCCATCTTGGCGCGGCTCGGATTGGGGGGCGGACATGACCTTGATGG 1749
294 ATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGAAT 343
|||||
1750 ATACAGAATTGCCATGAATGCGGCACTTCCGTCCTTCGCTCGTGTGGAAT 1799
344 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 393
|||||
1800 CGTTGGTAGGTGAGGGTCGACTGCGGGCGCCAGCTTCCCGAAGAGGTGAA 1849
394 AGCCCCGAGGATCCTCTAGAGTCCGATTTTCCGATGTCATCACCGGCGCG 443
|||
1850 AGCCCCGAG..... 1858

Fig. 5D

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1 ...CCTGCGCGGA.GGCCTCCGCACGGGCGTCAATTCTATGACTGGCTGT 46
|||
451 CCTCCTGCGCGGAGGGCCCTCGCACGGACGTCAATTCTATGACTGGCTGT 500
|||
47 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTANCG 96
|||
501 TCAACGTTGTGTATCCGGGACAAAAGGCGATGAGACCGGAGGACGTAGCG 550
|||
97 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 146
|||
551 GTGGCGGTGAGGTTGTATTGTGCGGAAGCTGTGCGCAGCGGGATTACGAC 600
|||
147 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 196
|||
601 GATCAACGAAAACGCCGATTTCGGCCATCTACCCAGGCAACATCGAGGCCG 650
|||
197 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 246
|||
651 CGATGGCGGTCTATGGTGAGGTGGGTGTGAGGGTCGTCTACGCCCGCATG 700
|||
247 TTCTTTGATCGGATGGACGGGCGCATTCAGGGTATGTGGACGCCTTGAA 296
|||
701 TTCTTTGATCGGATGGACGGGCGCATTCAGGGTATGTGGACGCCTTGAA 750
|||
297 GGCTCGCTCTCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 346
|||
751 GGCTCGCTCTCCCAAGTCGAACTGTGCTCGATCATGGAGGAAACGGCTG 800
|||
347 TGGCCAAAGATCGGATCACANCCCTGTCAGATCANTATCATGGCACGGCA 396
|||
801 TGGCCAAAGATCGGATCACAGCCCTGTCAGATCAGTATCATGGCACGGCA 850
|||
397 NGAGGTCCTATATCANTTTGGCCCGCTCCTGCCACTACCACNGCGGTGAC 446
:|||
851 GGAGGTCGTATATCAGTTTGGCCCGCTCCTGCCACTACCACGGCGGTGAC 900
|||
447 ATTTNAANGAATTCATNGGCACAA.CCTTCCCCCGTGATCNGGCGGTAA 495
|||
901 AGTTGAAGGAATGCGATGGGCACAAGCCTTCGCCCCGTGATCGGGCGGTAA 950
|||
496 TGTNGACCCA..... 505
|||
951 TGTGGACGCTTCACATGGCGGAGAGCGATCATGATGAGCGGATTCATGGG 1000
|||

Fig. 6

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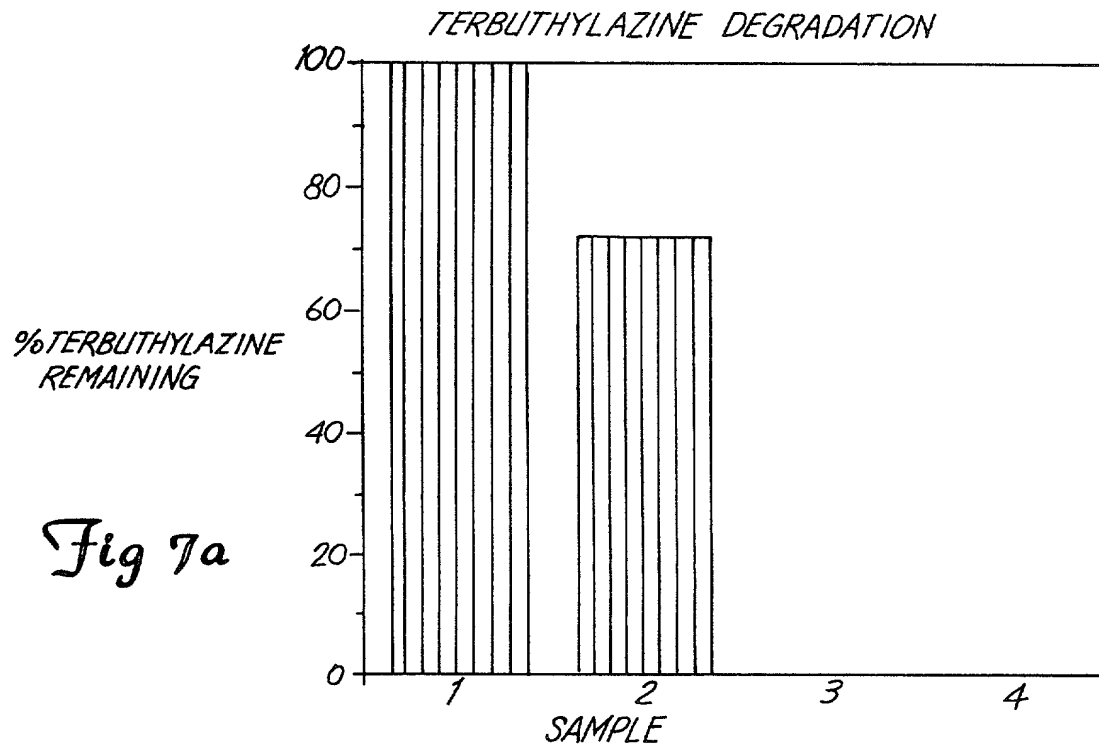


Fig 7a

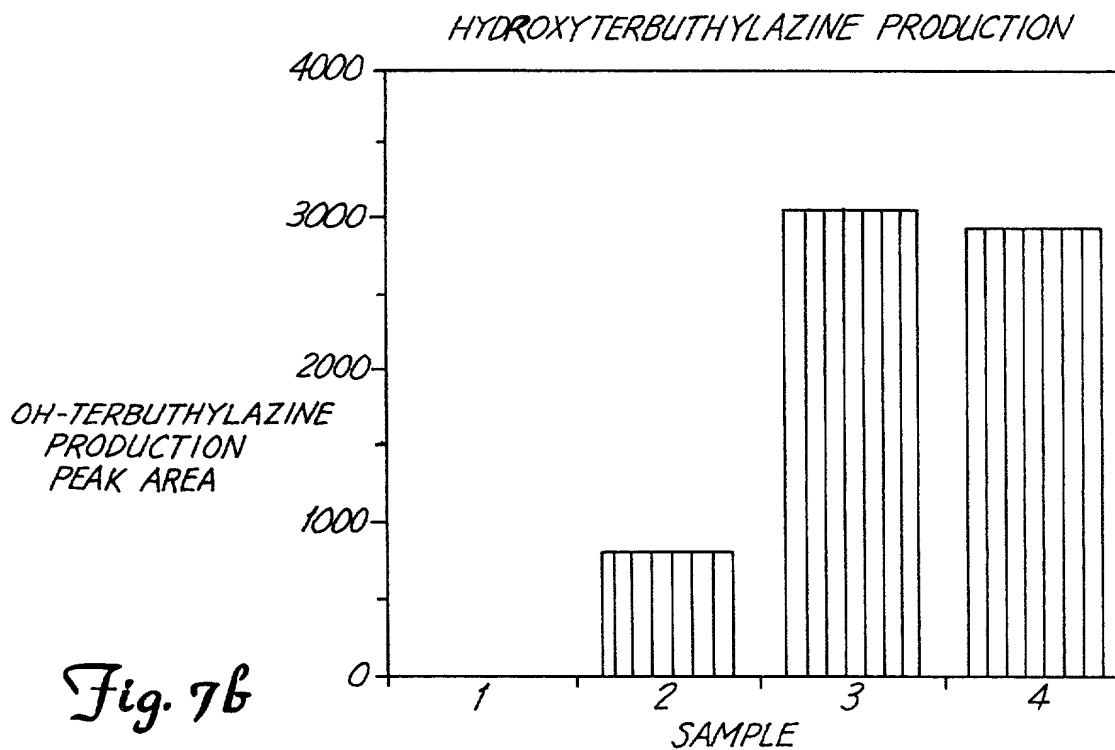


Fig. 7b

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TERBUTYLAZINE DEGRADATION BY SHUFFLED PROTEINS
A7, A11 AND T7 - 1 μ g/ml ptn conc
- EFFECT OF METAL IONS

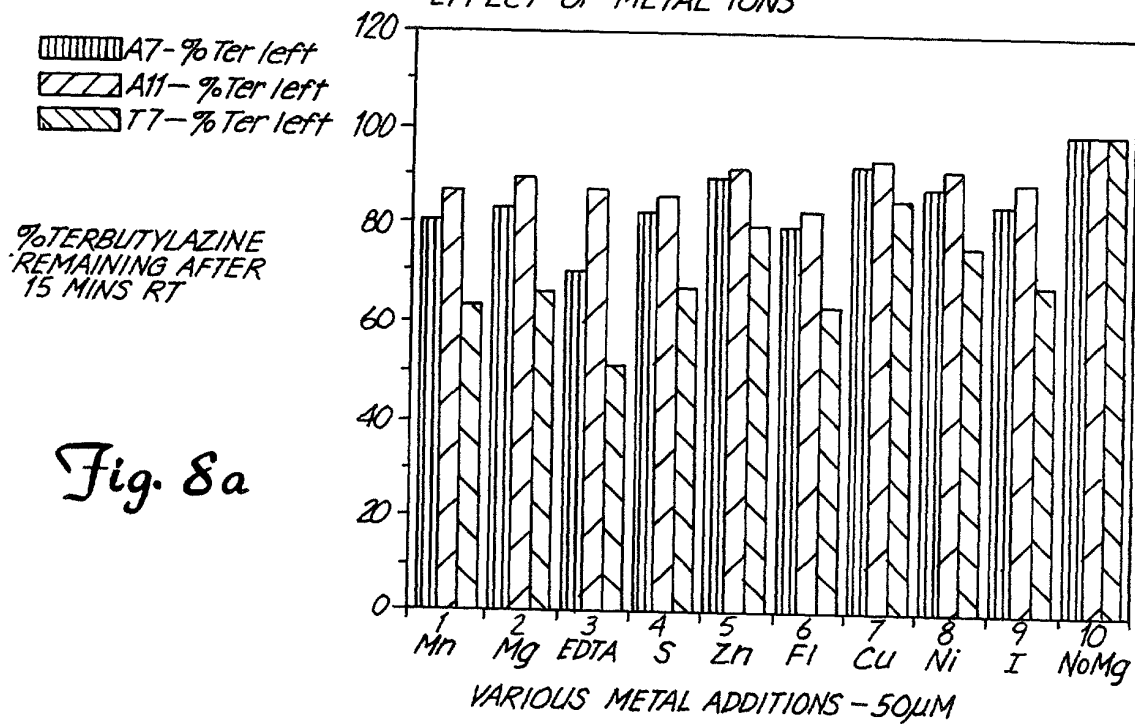


Fig. 8a

TERBUTYLAZINE DEGRADATION PRODUCT

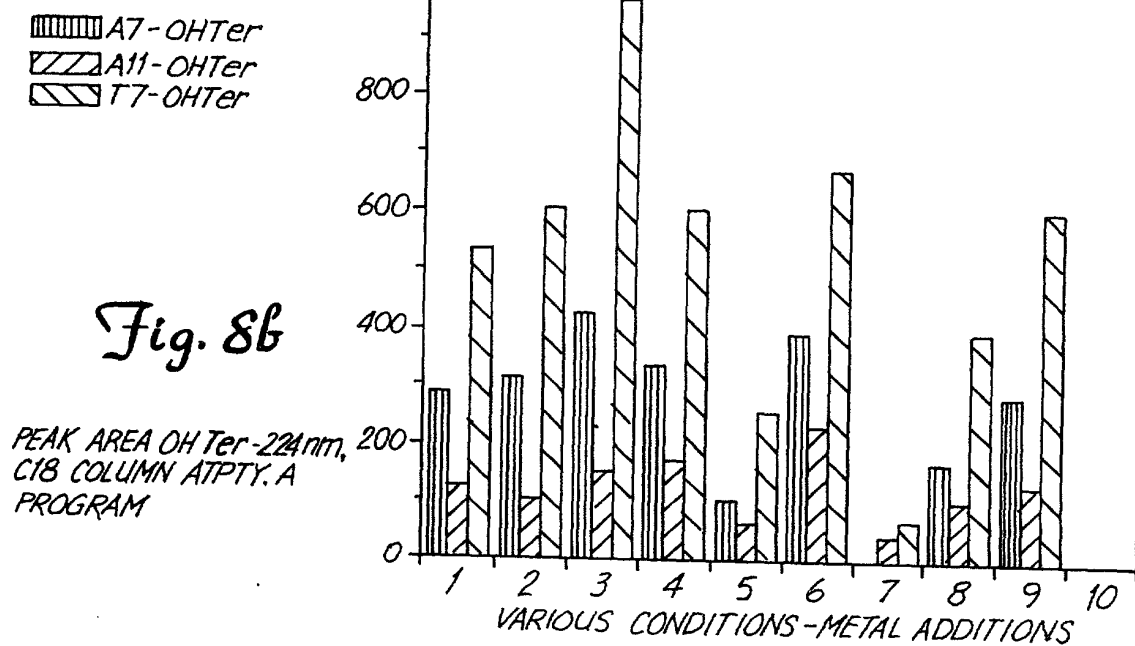


Fig. 8b

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Bacterium Translation of PCR amplified DNA sequence

	79	92			
ADP	SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
SG1	<u>PH</u> GRQ	FYDWLFNV <u>L</u> Y	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
M91-3	SHGRQ	FYDWLFNV <u>L</u> Y	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
J14a	<u>PH</u> GRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
38/38	SHGRQ	FYDWLFNV <u>L</u> Y	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
Clav.	SHGRQ	FYDWLFNVVY	PGQKAMRPED	VAVAVRLYCA	EAVRSGITTI
	125			170	
ADP	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
SG1	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
M91-3	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVD <u>T</u> LK
J14a	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
38/38	<u>NE</u> NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVD <u>T</u> LK
Clav.	NE.NADSAIY	PGNIEAAMAV	YGEVGVRVVY	ARMFFDRMDG	RIQGYVDALK
ADP	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
SG1	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
M91-3	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
J14a	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
38/38	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT
CLav.	ARSPQVELCS	IMEETAVAKD	RITALSDQYH	GTAGGRISVW	PAPATTTAVT

Fig. 9